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Sequence Listing could not be accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=11; day=20; hr=14; min=22; sec=45; ms=727;]

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Reviewer Comments:

<110> APPLICANT: SmithKline Beecham Biologicals
Ruelle, Jean-Louis

<120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides
from Neisseria Meningitidis

<130> FILE REFERENCE: BM45321

<140> CURRENT APPLICATION NUMBER:09700293

<141> CURRENT FILING DATE:2000-11-13

<150> PRIOR APPLICATION NUMBER: PCT/EP99/03255

<151> PRIOR FILING DATE: 1999-05-07

<150> PRIOR APPLICATION NUMBER: GB 9810276.7

<151> PRIOR FILING DATE: 1998-05-13

<160> NUMBER OF SEQ ID NOS: 6

<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1

<211> LENGTH: 1785

<212> TYPE: DNA

<213> ORGANISM: Bacteria

<400> SEQUENCE: 1

Per the above, please do not insert alpha numeric headings in the sequence. The above <213> response for sequence id# 1 is invalid, please insert genus/species response. Please correct the remaining sequences showing similar errors.

Application No: 09700293 Version No: 1.0

Input Set:

Output Set:

Started: 2008-10-27 13:37:45.658
Finished: 2008-10-27 13:37:46.171
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 513 ms
Total Warnings: 6
Total Errors: 0
No. of SeqIDs Defined: 6
Actual SeqID Count: 6

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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)

<110> APPLICANT: SmithKline Beecham Biologicals
Ruelle, Jean-Louis
<120> TITLE OF INVENTION: BASB029 Polynucleotides and Polypeptides
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<160> NUMBER OF SEQ ID NOS: 6
<170> SOFTWARE: FastSEQ for Windows Version 4.0

<210> SEQ ID NO 1
<211> LENGTH: 1785
<212> TYPE: DNA
<213> ORGANISM: Bacteria
<400> SEQUENCE: 1

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cccgtacaac gcaactgctgt cgtgttgagc ttccgttccg ataaagaagg cacgggagaa    240
aaagaagtta cagaagattc aaattgggga gtatatattcg acaagaaagg agtactaaca    300
gccggaacaa tcacctcaa agccggcgac aacctgaaaa tcaaacaaaa caccaatgaa    360
aacaccaatg ccagtagctt cacctactcg ctgaaaaaag acctcacaga tctgaccagt    420
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accaaaggct tgaatttcgc gaaaaaaacg gctgagacca acggcgacac cacggttcat    540
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cgtgcgggca tcgccaagc gattgcaacc gcaggtctgg ttcaggcgta tctgcccggc   1620
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tactcaagca tttccgacgg cggaattgg attatcaaag gcacggcttc cggcaattcg   1740
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<212> TYPE: PRT
<213> ORGANISM: Bacteria
<400> SEQUENCE: 2
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20	25	30	
Thr Val Ala Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln			
35	40	45	
Ala Ser Thr Thr Asp Asp Asp Asp Leu Tyr Leu Glu Pro Val Gln Arg			
50	55	60	
Thr Ala Val Val Leu Ser Phe Arg Ser Asp Lys Glu Gly Thr Gly Glu			
65	70	75	80
Lys Glu Val Thr Glu Asp Ser Asn Trp Gly Val Tyr Phe Asp Lys Lys			
85	90	95	
Gly Val Leu Thr Ala Gly Thr Ile Thr Leu Lys Ala Gly Asp Asn Leu			
100	105	110	
Lys Ile Lys Gln Asn Thr Asn Glu Asn Thr Asn Ala Ser Ser Phe Thr			
115	120	125	
Tyr Ser Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu			
130	135	140	
Lys Leu Ser Phe Ser Ala Asn Ser Asn Lys Val Asn Ile Thr Ser Asp			
145	150	155	160
Thr Lys Gly Leu Asn Phe Ala Lys Lys Thr Ala Glu Thr Asn Gly Asp			
165	170	175	
Thr Thr Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu			
180	185	190	
Leu Asn Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp			
195	200	205	
Asp Glu Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly			
210	215	220	
Trp Asn Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val			
225	230	235	240
Asp Phe Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr			
245	250	255	
Lys Thr Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Arg Thr			
260	265	270	
Glu Val Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly			
275	280	285	
Lys Leu Val Thr Gly Lys Asp Lys Gly Glu Asn Asp Ser Ser Thr Asp			
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Lys Gly Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn			
305	310	315	320
Lys Ala Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly			
325	330	335	
Gln Ala Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe			
340	345	350	
Ala Ser Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly			
355	360	365	
Asn Ile Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val			
370	375	380	
Asn Gln Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala			
385	390	395	400
Gly Ser Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly			
405	410	415	
Lys Met Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile			
420	425	430	
Thr Arg Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln			
435	440	445	
Phe Ser Ser Val Ser Leu Gly Ala Gly Ala Asp Ala Pro Thr Leu Ser			
450	455	460	

Val Asp Asp Glu Gly Ala Leu Asn Val Gly Ser Lys Asp Ala Asn Lys
465 470 475 480
Pro Val Arg Ile Thr Asn Val Ala Pro Gly Val Lys Glu Gly Asp Val
485 490 495
Thr Asn Val Ala Gln Leu Lys Gly Val Ala Gln Asn Leu Asn Asn His
500 505 510
Ile Asp Asn Val Asp Gly Asn Ala Arg Ala Gly Ile Ala Gln Ala Ile
515 520 525
Ala Thr Ala Gly Leu Val Gln Ala Tyr Leu Pro Gly Lys Ser Met Met
530 535 540
Ala Ile Gly Gly Gly Thr Tyr Arg Gly Glu Ala Gly Tyr Ala Ile Gly
545 550 555 560
Tyr Ser Ser Ile Ser Asp Gly Gly Asn Trp Ile Ile Lys Gly Thr Ala
565 570 575
Ser Gly Asn Ser Arg Gly His Phe Gly Ala Ser Ala Ser Val Gly Tyr
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Gln Trp

<210> SEQ ID NO 3

<211> LENGTH: 1776

<212> TYPE: DNA

<213> ORGANISM: Bacteria

<400> SEQUENCE: 3

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tatttagacc	ccgtacaacg	cactgttgcc	gtgttgatag	tcaattccga	taaagaaggc	240	
acgggagaaa	aagaaaaagt	agaagaaaat	tcagattggg	cagtatatatt	caacgagaaa	300	
ggagtactaa	cagccagaga	aatcacctc	aaagccggcg	acaacctgaa	aatcaaacaa	360	
aacgacacaa	acttcaccta	ctcgctgaaa	aaagacctca	cagatctgac	cagtgttgga	420	
actgaaaaat	tatcgtttag	cgcaaacggc	aataaagtca	acatcacaag	cgacaccaa	480	
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gcaggctgga	acattaaagg	cgttaaaccc	ggtacaacag	cttccgataa	cgttgatttc	720	
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attaaagaaa	aagacggtaa	ggttggtact	ggtaaagaca	aaggcgagaa	tggttcttct	900	
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attaccaatg	tcgccccggg	cgttaaagag	ggggatgtta	caaacgtcgc	acaacttaa	1500	
ggcgtggcgc	aaaacttgaa	caaccgcatc	gacaatgtgg	acggcaacgc	gcgtgcgggc	1560	
atcgcccaag	cgattgcaac	cgcaggtctg	gttcaggcgt	atttgcccg	caagagtatg	1620	
atggcgatcg	gcggcggcac	ttatcgcggc	gaagcgggtt	acgccatcg	ctactccagt	1680	
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<210> SEQ ID NO 4

<211> LENGTH: 591

<212> TYPE: PRT

<213> ORGANISM: Bacteria

<400> SEQUENCE: 4

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 20             25             30
Thr Val Lys Thr Ala Val Leu Ala Thr Leu Leu Phe Ala Thr Val Gln
 35             40             45
Ala Ser Ala Asn Asn Glu Glu Gln Glu Glu Asp Leu Tyr Leu Asp Pro
 50             55             60
Val Gln Arg Thr Val Ala Val Leu Ile Val Asn Ser Asp Lys Glu Gly
 65             70             75             80
Thr Gly Glu Lys Glu Lys Val Glu Glu Asn Ser Asp Trp Ala Val Tyr
 85             90             95
Phe Asn Glu Lys Gly Val Leu Thr Ala Arg Glu Ile Thr Leu Lys Ala
 100            105            110
Gly Asp Asn Leu Lys Ile Lys Gln Asn Gly Thr Asn Phe Thr Tyr Ser
 115            120            125
Leu Lys Lys Asp Leu Thr Asp Leu Thr Ser Val Gly Thr Glu Lys Leu
 130            135            140
Ser Phe Ser Ala Asn Gly Asn Lys Val Asn Ile Thr Ser Asp Thr Lys
 145            150            155            160
Gly Leu Asn Phe Ala Lys Glu Thr Ala Gly Thr Asn Gly Asp Thr Thr
 165            170            175
Val His Leu Asn Gly Ile Gly Ser Thr Leu Thr Asp Thr Leu Leu Asn
 180            185            190
Thr Gly Ala Thr Thr Asn Val Thr Asn Asp Asn Val Thr Asp Asp Glu
 195            200            205
Lys Lys Arg Ala Ala Ser Val Lys Asp Val Leu Asn Ala Gly Trp Asn
 210            215            220
Ile Lys Gly Val Lys Pro Gly Thr Thr Ala Ser Asp Asn Val Asp Phe
 225            230            235            240
Val Arg Thr Tyr Asp Thr Val Glu Phe Leu Ser Ala Asp Thr Lys Thr
 245            250            255
Thr Thr Val Asn Val Glu Ser Lys Asp Asn Gly Lys Lys Thr Glu Val
 260            265            270
Lys Ile Gly Ala Lys Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu
 275            280            285
Val Thr Gly Lys Asp Lys Gly Glu Asn Gly Ser Ser Thr Asp Glu Gly
 290            295            300
Glu Gly Leu Val Thr Ala Lys Glu Val Ile Asp Ala Val Asn Lys Ala
 305            310            315            320
Gly Trp Arg Met Lys Thr Thr Thr Ala Asn Gly Gln Thr Gly Gln Ala
 325            330            335
Asp Lys Phe Glu Thr Val Thr Ser Gly Thr Asn Val Thr Phe Ala Ser
 340            345            350
Gly Lys Gly Thr Thr Ala Thr Val Ser Lys Asp Asp Gln Gly Asn Ile
 355            360            365
Thr Val Met Tyr Asp Val Asn Val Gly Asp Ala Leu Asn Val Asn Gln
 370            375            380
Leu Gln Asn Ser Gly Trp Asn Leu Asp Ser Lys Ala Val Ala Gly Ser
 385            390            395            400
Ser Gly Lys Val Ile Ser Gly Asn Val Ser Pro Ser Lys Gly Lys Met
 405            410            415
Asp Glu Thr Val Asn Ile Asn Ala Gly Asn Asn Ile Glu Ile Thr Arg
 420            425            430
Asn Gly Lys Asn Ile Asp Ile Ala Thr Ser Met Thr Pro Gln Phe Ser
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435	440	445
Ser Val Ser Leu Gly Ala Gly	Ala Asp Ala Pro Thr Leu Ser Val Asp	
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Gly Asp Ala Leu Asn Val Gly	Ser Lys Lys Asp Asn Lys Pro Val Arg	
465	470	475
Ile Thr Asn Val Ala Pro Gly	Val Lys Glu Gly Asp Val Thr Asn Val	
485	490	495
Ala Gln Leu Lys Gly Val Ala	Gln Asn Leu Asn Asn Arg Ile Asp Asn	
500	505	510
Val Asp Gly Asn Ala Arg Ala	Gly Ile Ala Gln Ala Ile Ala Thr Ala	
515	520	525
Gly Leu Val Gln Ala Tyr Leu	Pro Gly Lys Ser Met Met Ala Ile Gly	
530	535	540
Gly Gly Thr Tyr Arg Gly Glu	Ala Gly Tyr Ala Ile Gly Tyr Ser Ser	
545	550	555
Ile Ser Asp Gly Gly Asn Trp	Ile Ile Lys Gly Thr Ala Ser Gly Asn	
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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide
 <400> SEQUENCE: 5
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36

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 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Oligonucleotide
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34